

OIIPE

RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/750,240

TIME: 11:09:45

Input Set : A:\220002056723.txt

Output Set: N:\CRF3\11062001\I750240.raw

4 <110> APPLICANT: Hammon, H. K.
5 Insel, P. A.
6 Ping, P.
7 Post, S. R.
8 Gao, M.
10 <120> TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
11 FAILURE
13 <130> FILE REFERENCE: 220002056723
15 <140> CURRENT APPLICATION NUMBER: US 09/750,240
C--> 16 <141> CURRENT FILING DATE: 2001-10-12 *OK*
18 <150> PRIOR APPLICATION NUMBER: US 09/472,667
19 <151> PRIOR FILING DATE: 1999-12-27
21 <150> PRIOR APPLICATION NUMBER: US 09/008,097 ✓
22 <151> PRIOR FILING DATE: 1998-01-16
24 <150> PRIOR APPLICATION NUMBER: US 08/924,757 ✓
25 <151> PRIOR FILING DATE: 1997-09-05
27 <150> PRIOR APPLICATION NUMBER: US 60/048,933
28 <151> PRIOR FILING DATE: 1997-06-16
30 <150> PRIOR APPLICATION NUMBER: US 08/708,661
31 <151> PRIOR FILING DATE: 1996-09-05
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35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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38 <211> LENGTH: 314
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
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43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (1)...(314)
45 <223> OTHER INFORMATION: n = A,T,C or G
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49 gaacgcaatg ggcagaagcg ttcgcggcgc cgtggcactc gggcaggtgg cttctgcacg 120
50 ccccgctata tgagctgcct ccgggatgca gagccacca gccccacccc tgcggggcccc 180
W--> 51 cctcgggtgcc cctggcagga tgacgccttc atccggaggg gcggcccang caagggcaag ✓ 240
52 gaactggggc tgcgggcagt ggccctgggc ttcgaagata ccgaagtgc aacgacaccg 300
53 gcgggaccgc tgaa 314
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56 <211> LENGTH: 104
57 <212> TYPE: PRT
58 <213> ORGANISM: Homo sapiens
60 <220> FEATURE:
61 <221> NAME/KEY: VARIANT
62 <222> LOCATION: (1)...(104)
63 <223> OTHER INFORMATION: Xaa = Any Amino Acid
65 <400> SEQUENCE: 2
66 Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys

ENTERED

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67 1          5          10          15
68 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Gly
69          20          25          30
70 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
71          35          40          45
72 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
73          50          55          60
W--> 74 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys OK
75 65          70          75          80
76 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
77          85          90          95
78 Thr Thr Thr Pro Ala Gly Pro Leu
79          100
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82 <211> LENGTH: 1812
83 <212> TYPE: DNA
84 <213> ORGANISM: Homo sapiens
86 <400> SEQUENCE: 3
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88 ccgcgcagcc cctctgcggg cctctggtgc cctgtgttct ttgtatacat cgcatacacg 120
89 ctccctccca tccgcagtcg ggctgcgctc ctacagcgcc tgggcctctc cacttgcat 180
90 ttgatcttgg cctggcaact taaccgtggt gatgccttcc tctggaagca gctcggtgcc 240
91 aatgtgtctg tgttctctcg caccaacgtc attagcatct gcacacacta tccagcagag 300
92 gtgtctcagc gccaggcctt tcaggagacc cgcagttaca tccaggcccg gctccacctg 360
93 cagcatgaga atcggcagca ggagcggtcg ctgctgtcgg tattgcccc gacggttgcc 420
94 atggagatga aagaagacat caacacaaaa aaagaagaca tgttccaca gatctacata 480
95 cagaagcatg acaatgtcag catcctgttt gcagacattg agggcttcac cagcctggca 540
96 tccagtgca ctgcgcagga gctggtcatg accctgaatg agctctttgc ccggtttgac 600
97 aagctggctg cggagaatca ctgcctgagg atcaagatct tgggggactg ttactactgt 660
98 gtgtcagggc tgcggaggc ccgggcccgc catgcccact gctgtgtgga gatgggggta 720
99 gacatgattg aggccatctc gctggtacgt gaggtgacag gtgtgaatgt gaacatgcgc 780
100 gtgggcatcc acagcgggcg cgtgcactgc ggcgtccttg gcttgcgga atggcagttc 840
101 gatgtgtggt ccaatgatgt gaccctggcc aaccacatgg aagcaggaag ccgggctggc 900
102 cgcattccca tcaactgggc aacactgcag taactgaacg gggactacga agtggagcca 960
103 ggcgtggtg gcaagcgcaa cgcgtacctc aaggagcagc acattgagac ttctctcatc 1020
104 ctgggcgcca gccagaaacg gaaagaggag aaaggcatgc tggccaagct gcagcggact 1080
105 cgggccaact ccatggaagg gctgatgccg cgatgggttc ctgacgtgc cttctcccgg 1140
106 accaaggact ccaaggcctt ccgccagatg ggcattgatg attccagcaa agacaaccgg 1200
107 ggcacccaag atgccctgaa cctgaggat gaggtggatg agttcctgag ccgtgccatc 1260
108 gatgcccgca gcattgatca gctgcggaag gaccatgtgc gccggttttt gctcaccttc 1320
109 cagagagagg attttgagaa gaagtactcc cggaagggtg atccccgctt cggagcctac 1380
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111 cactccaccc tgatgcttgg gatttatgcc agcatcttcc tgetgctgct aatcacctg 1500
112 ctgatctgtg ctgtgtactc ctgtggttct ctgttcccta aggccttgc acgtctgtcc 1560
113 cgcagcattg tccgctcacg ggcacatagc accgcagttg gcattctttc cgtcctgctt 1620
114 gtgtttactt ctgccattgc caacatgttc acctgtaacc acacccccat acggagctgt 1680
115 gcagcccgga tgctgaattt aacacctgct gacatcactg cctgccacct gcagcagctc 1740
116 aattactctc tgggcctgga tgctcccctg tgtgagggca ccatgcccac ctgcagcttt 1800
117 cctgaggtgt tc 1812

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119 <210> SEQ ID NO: 4
120 <211> LENGTH: 604
121 <212> TYPE: PRT
122 <213> ORGANISM: Homo sapiens
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127 Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val
128 20 25 30
129 Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala
130 35 40 45
131 Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala
132 50 55 60
133 Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
134 65 70 75 80
135 Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
136 85 90 95
137 Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
138 100 105 110
139 Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu
140 115 120 125
141 Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys
142 130 135 140
143 Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile
144 145 150 155 160
145 Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe
146 165 170 175
147 Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu
148 180 185 190
149 Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys
150 195 200 205
151 Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu
152 210 215 220
153 Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val
154 225 230 235 240
155 Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn
156 245 250 255
157 Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val
158 260 265 270
159 Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr
160 275 280 285
161 Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile
162 290 295 300
163 Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro
164 305 310 315 320
165 Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu
166 325 330 335
167 Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly
168 340 345 350

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169 Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu
170      355      360      365
171 Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser
172      370      375      380
173 Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg
174 385      390      395      400
175 Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu
176      405      410      415
177 Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His
178      420      425      430
179 Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys
180      435      440      445
181 Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala
182      450      455      460
183 Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro
184 465      470      475      480
185 His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu
186      485      490      495
187 Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
188      500      505      510
189 Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
190      515      520      525
191 His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
192      530      535      540
193 Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
194 545      550      555      560
195 Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
196      565      570      575
197 Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu
198      580      585      590
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203 <211> LENGTH: 3549
204 <212> TYPE: DNA
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210 cccgcgtata tgagctgcct ccgggatgca gagccacca gcccacccc tgcgggcccc      180
211 cctcggtgcc cctggcagga tgacgccttc atccggaggg gcggcccagg caagggcaag      240
212 gagctggggc tgcgggcagt ggccctgggc ttcaggata ccgaggtgac aacgacagcg      300
213 ggcgggacgg ctgaggtggc gcccgcgcgc gtgccagga gtgggcgatc ctgctggcgc      360
214 cgtttggtgc aggtgttcca gtcgaagcag ttccgttcgg ccaagctgga gcgcctgtac      420
215 cagcgggtact ttttcagat gaaccagagc agcctgacgc tgctgggtggc ggtgctgggtg      480
216 ctgctcacag cgggtgctgt ggctttccaa gccgcaccgc cccgcctca gcctgcctat      540
217 gtggcactgt tggcctgtgc cgcgcacctg ttctggtggc tcatggtggt gtgtaaccgg      600
218 catagcttcc gccaggactc catgtgggtg gtgagtaacg tgggtgctggg catcctggcg      660
219 gcagtgcagg tcgggggcgc tttcgcagca gaccgcgcga gccctctgc gggcctctgg      720

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222	ggtgatgcct	tctcttgaa	gcagctcggt	gccaatgtgc	tgtgttctct	ctgcaccaac	900
223	gtcattagca	tctgcacaca	ctatccagca	gaggtgtctc	agcgccaggc	ctttcaggag	960
224	acccgcagtt	acatccaggc	ccggctccac	ctgcagcatg	agaatcggca	gcaggagcgg	1020
225	ctgctgctgt	cggtattgcc	ccagcacggt	gccatggaga	tgaagaaga	catcaacaca	1080
226	aaaaaagaag	acatgttcca	caagatctac	atacagaagc	atgacaatgt	cagcatcctg	1140
227	tttgagaca	ttgagggtct	caccagcctg	gcattcccag	gcactgcgca	ggagctggtc	1200
228	atgaccctga	atgagctctt	tgcctgggtt	gacaagctgg	ctgaggagaa	tactgcctg	1260
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233	gccaaccaca	tgggaagcag	aagccgggct	ggccgcatcc	acatcactcg	ggcaacactg	1560
234	cagtacctga	acggggacta	cgaagtggag	ccaggccctg	gtggcaagcg	caacgcgtac	1620
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236	gagaaaggca	tgttgccaa	gctgcagcgg	actcgggcca	actccatgga	agggctgatg	1740
237	ccgcgatggg	ttcctgatcg	tgccttctct	cggaccaagg	actccaaggc	cttcggccag	1800
238	atgggcattg	atgattccag	caaagacaac	cggggcaccc	aagatgccct	gaacctgtag	1860
239	gatgaggtgg	atgagttcct	gagccgtgcc	atcgatgccc	gcagcattga	tcagctgcgg	1920
240	aaggaccatg	tgcgcgggtt	ttgtctcacc	ttccagagag	aggattttga	gaagaagtac	1980
241	tcccgggaag	tggatccccg	cttcggagcc	tacgttgcc	gtgccctggt	ggtcttctgc	2040
242	ttcatctgct	tcattccagct	tctaattttc	ccacactcca	ccctgatgct	tgggatttat	2100
243	gccagcatct	tcctgctgct	gctaattcacc	gtgctgatct	gtgctgtgta	ctcctgtggt	2160
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246	ttcacctgta	accacacccc	catacggagc	tgtgcagccc	ggatgctgaa	tttaacacct	2340
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263	ccacagtatg	acatctgggg	gaacacagtg	aatgtctcta	gtcgtatgga	cagcacgggg	3360
264	gtccccgacc	gaatccagg	gaccacggac	ctgtaccagg	ttctagctgc	caagggtac	3420
265	cagctggagt	gtcaggggt	ggtcaagggt	aagggaagg	gggagatgac	cacctacttc	3480
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269	<210>	SEQ ID NO: 6					

VERIFICATION SUMMARY

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DATE: 11/06/2001

TIME: 11:09:46

Input Set : A:\220002056723.txt

Output Set: N:\CRF3\11062001\I750240.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2